

1/9

## SEQUENCE LISTING

<110> GEMMA BIOTECHNOLOGY LTD.; JULIUS, Michael H.; FILIPP, Dominik  
<120> THE INDUCTION OF ANTIBIOTIC PROTEINS AND PEPTIDES BY  
LAIT/sCD14-PROTEIN  
<130> 47841/00048  
<140> PCT/CA99/00482  
<141> 1999-05-27  
<150> US 60/086,884  
<151> 1998-05-27  
<160> 8  
<170> Wordperfect 6.1  
<210> 1  
<211> 1122  
<212> DNA  
<213> bovine  
  
<400> 1  
atggtgtgcg tgccctaccc gctgctgctg ctgctgccgt cactgctgcg tgtgtctgcg 60  
gacacaacag aaccctgcga gctggacgac gacgattcc gttgtgtctg caacttcacg 120  
gatccgaagc ctgactggtc tagcgccgtt cagtgtatgg ttgcccgtcga ggtggagatc 180  
agtgccggcg gccgcagcct ggaacagttt ctcaaggag ccgacaccaa cccgaagcag 240  
tatgctgaca caatcaaggc tctgcgcgtt cggcgactca agctggcgc tgcacaggtt 300  
cctgctcagc ttctggtcgc cgttctgcgc gcgctcggtt actctcgct caaggaactg 360  
acgcttgagg acctggaggt aaccggccca acgccccga cgcctctgga agccgctggg 420  
cctgcgcctca ccaccctcag tctgcgttaac gtatcggtt caacaggagg tgcctggcgc 480  
ggcgaaactgc agcagttggct caagcctggg ctcagggtgc tgaacattgc ccaagcacac 540  
tcgcttgcct ttccgtgcgc agggctctcc accttcgagg cgctcaccac cctagacctg 600  
tctgacaatc ccagtctcgg cgacacgggg ctgatggcag ctctctgtcc gaacaagttc 660  
ccggccctcc aatatcttagc gctacgcaac gcggggatgg agacgcccag cggcgtgtgc 720  
gcggcgctgg cggcagcggag ggtgcagccc caaagcctgg acctcagcca caactcgctg 780  
cgcgtaaccg cccccgggtgc taccggatgt gtctggccca gtgcactaag gtctctcaat 840  
ttgtcggtcg ctgggctgga gcaagtgcct aagggactgc cccctaagct cagcgtgttt 900  
gatctcagct gcaacaagct aagcagggag cgcggcggag acgagctgcc cgaggtaaat 960  
gacctgactc tggacggaaa tcccttctg gaccctggag ccccccagca caaaaatgac 1020  
ccgatgatct ccggcggtgtt cccagcctgt ggcgttctg cttgaccat ggggggtgtca 1080  
ggagccctgg cgctgcttca aggagcccga ggcttcgcgt aa 1122

2/9

<210>	2	
<211>	1128	
<212>	DNA	
<213>	human	
 <400>	2	
atggagcgcg cgtcctgctt gttgctgctg ctgctgccgc tgggtcacgt ctctgcgacc	60	
acggccagaac cttgtgagct ggacgatgaa gatttccgct gcgtctgcaa cttctccgaa	120	
cctcagccccg actggtcgca agccttccag tgtgtgtctg cagtagaggt ggagatccat	180	
gccggcggtc tcaaacctaga gccgtttcta aagcgcgtcg atgcggacgc cgaccgcgg	240	
cagtatgctg acacggtcaa ggctctccgc gtgcggcggc tcacagtggg agccgcacag	300	
gttccctgctc agctactgggt aggcgcctcg cgtgtgtctag cgtactcccg cctcaaggaa	360	
ctgacgctcg aggacctaaa gataaccggc accatgcctc cgctgcctct ggaagccaca	420	
ggacttgcac ttccagctt gcgcctacgc aacgtgtcgt gggcgacagg gcgttcttgg	480	
ctcgccgagc tgcagcgtg gctcaagcca ggcctcaagg tactgagcat tgcccaagca	540	
cactcgccctg cttttctcg cgaacaggtt cgcgccttcc cggcccttac cagcctagac	600	
ctgtctgaca atcctggact gggcgaacgc ggactgtatgg cggctctctg tccccacaag	660	
ttcccgggcca tccagaatct agcgctgcgc aacacaggaa tggagacgccc cacaggcgtg	720	
tgcgcgcac tggcgccggc aggtgtgcag ccccacagcc tagacctcag ccacaactcg	780	
ctgcgcgcac ccgtaaaccc tagcgctccg agatgcatgt ggtccagcgc cctgaactcc	840	
ctcaatctgt cgttcgctgg gcttggAACAG gtgcctaaag gactgccagc caagctcaga	900	
gtgctcgatc tcaagctgcaa cagactgaac agggcgccgc agcctgacga gctgcccag	960	
gtggataacc tgacactgga cgggaatccc ttccctggtcc ctggaaactgc cctccccac	1020	
gaggcctcaa tgaactccgg cgtgggtccca gcctgtgcac gttcgaccct gtcgggtgggg	1080	
gtgtcgggaa ccctggtgct gctccaagggg gcccggggct ttgcctaa	1128	

<210>	3	
<211>	1101	
<212>	DNA	
<213>	murine	
 <400>	3	
ATGGAGCGTG TGCTTGGCTT GTTGCTGTTG CTTCTGGTGC ACGCCTCTCC CGCCCCACCA	60	
GAGCCCTGCG AGCTAGACGA GGAAAGTTGT TCCTGCAACT TCTCAGATCC GAAGCCAGAT	120	
TGGTCCAGCG CTTCATTG TTTGGGGCG GCAGATGTGG AATTGTACGG CGGGGGCCGC	180	
AGCCTGGAAT ACCTTCTAAA GCGTGTGGAC ACGGAAGCAG ATCTGGGGCA GTTCACTGAT	240	
ATTATCAAGT CTCTGTCTT AAAGCGGCTT ACGGTGCGGG CCGCGCGGAT TCCTAGTCGG	300	
ATTCTATTAG GAGCCCTGCG TGTGCTCGGG ATTTCCGGCC TCCAGGAACT GACTCTTGAA	360	

3/9

AATCTCGAGG	TAACCGGCAC	CGCGCCGCCA	CCGCTTCTGG	AAGCCACCGG	ACCCGATCTC	420
AACATCTTGA	ACCTCCGCAA	CGTGTCTGG	GCAACAAGGG	ATGCCTGGCT	CGCAGAACTG	480
CAGCAGTGGC	TAAAGCCTGG	ACTCAAGGTA	CTGAGTATTG	CCCAAGCACA	CTCACTCAAC	540
TTTCCTGCG	AACAGGTCCG	CGTCTTCCCT	GCCCTCTCCA	CCTTAGACCT	GTCTGACAAT	600
CCTGAATTGG	GCGAGAGAGG	ACTGATCTCA	GCCCTCTGTC	CCCTCAAGTT	CCCGACCCTC	660
CAAGTTTAG	CGCTGCGTAA	CGCGGGGATG	GAGACGCCA	GCGGCGTGTG	CTCTGCGCTG	720
GCCGCAGCAA	GGGTACAGCT	GCAAGGACTA	GACCTTAGTC	ACAATTCACT	GCAGGGATGCT	780
GCAGGCGCTC	CGAGTTGTGA	CTGGCCCAGT	CAGCTAAACT	CGCTCAATCT	GTCTTTCACT	840
GGGCTGAAGC	AGGTACCTAA	AGGGCTGCCA	GCCAAGCTCA	GCGTGCTGGA	TCTCAGTTAC	900
AACAGGCTGG	ATAGGAACCC	TAGCCCAGAT	GAGCTGCC	AAGTGGGGAA	CCTGTCAC	960
AAAGGAAATC	CCTTTTGGA	CTCTGAATCC	CACTCGGAGA	AGTTAACTC	TGGCGTAGTC	1020
ACCGCCGGAG	CTCCATCATC	CCAAGCAGTG	GCCTTGTCA	GAACCTCTGGC	TTTGCTCCTA	1080
GGAGATCGCC	TCTTGTTTA	A				1101

<210>	4		
<211>	3738		
<212>	PRT		
<213>	bovine		
<400>	4		
Met Val Cys Val Pro Tyr Leu Leu Leu Leu Leu Pro Ser Leu Leu			
1	5	10	15
Arg Val Ser Ala Asp Thr Thr Glu Pro Cys Glu Leu Asp Asp Asp Asp			
20	25	30	
Phe Arg Cys Val Cys Asn Phe Thr Asp Pro Lys Pro Asp Trp Ser Ser			
35	40	45	
Ala Val Gln Cys Met Val Ala Val Glu Val Glu Ile Ser Ala Gly Gly			
50	55	60	
Arg Ser Leu Glu Gln Phe Leu Lys Gly Ala Asp Thr Asn Pro Lys Gln			
65	70	75	80
Tyr Ala Asp Thr Ile Lys Ala Leu Arg Val Arg Arg Leu Lys Leu Gly			
85	90	95	
Ala Ala Gln Val Pro Ala Gln Leu Leu Val Ala Val Leu Arg Ala Leu			
100	105	110	
Gly Tyr Ser Arg Leu Lys Glu Leu Thr Leu Glu Asp Leu Glu Val Thr			
115	120	125	
Gly Pro Thr Pro Pro Thr Pro Leu Glu Ala Ala Gly Pro Ala Leu Thr			
130	135	140	
Thr Leu Ser Leu Arg Asn Val Ser Trp Thr Thr Gly Gly Ala Trp Leu			
145	150	155	160

4/9

Gly Glu Leu Gln Gln Trp Leu Lys Pro Gly Leu Arg Val Leu Asn Ile  
 165 170 175

Ala Gln Ala His Ser Leu Ala Phe Pro Cys Ala Gly Leu Ser Thr Phe  
 180 185 190

Glu Ala Leu Thr Thr Leu Asp Leu Ser Asp Asn Pro Ser Leu Gly Asp  
 195 200 205

Thr Gly Leu Met Ala Ala Leu Cys Pro Asn Lys Phe Pro Ala Leu Gln  
 210 215 220

Tyr Leu Ala Leu Arg Asn Ala Gly Met Glu Thr Pro Ser Gly Val Cys  
 225 230 235 240

Ala Ala Leu Ala Ala Ala Arg Val Gln Pro Gln Ser Leu Asp Leu Ser  
 245 250 255

His Asn Ser Leu Arg Val Thr Ala Pro Gly Ala Thr Arg Cys Val Trp  
 260 265 270

Pro Ser Ala Leu Arg Ser Leu Asn Leu Ser Phe Ala Gly Leu Glu Gln  
 275 280 285

Val Pro Lys Gly Leu Pro Pro Lys Leu Ser Val Leu Asp Leu Ser Cys  
 290 295 300

Asn Lys Leu Ser Arg Glu Pro Arg Arg Asp Glu Leu Pro Glu Val Asn  
 305 310 315 320

Asp Leu Thr Leu Asp Gly Asn Pro Phe Leu Asp Pro Gly Ala Leu Gln  
 325 330 335

His Gln Asn Asp Pro Met Ile Ser Gly Val Val Pro Ala Cys Ala Arg  
 340 345 350

Ser Ala Leu Thr Met Gly Val Ser Gly Ala Leu Ala Leu Leu Gln Gly  
 355 360 365

Ala Arg Gly Phe Ala  
 370

<210> 5  
<211> 375  
<212> PRT  
<213> human

<400> 5  
Met Glu Arg Ala Ser Cys Leu Leu Leu Leu Leu Pro Leu Val His  
1 5 10 15

Val Ser Ala Thr Thr Pro Glu Pro Cys Glu Leu Asp Asp Glu Asp Phe  
20 25 30

Arg Cys Val Cys Asn Phe Ser Glu Pro Gln Pro Asp Trp Ser Glu Ala  
35 40 45

Phe Gln Cys Val Ser Ala Val Glu Val Glu Ile His Ala Gly Gly Leu  
50 55 60

Asn Leu Glu Pro Phe Leu Lys Arg Val Asp Ala Asp Ala Asp Pro Arg  
65 70 75 80

5/9

Gln Tyr Ala Asp Thr Val Lys Ala Leu Arg Val Arg Arg Leu Thr Val  
85 90 95

Gly Ala Ala Gln Val Pro Ala Gln Leu Leu Val Gly Ala Leu Arg Val  
100 105 110

Leu Ala Tyr Ser Arg Leu Lys Glu Leu Thr Leu Glu Asp Leu Lys Ile  
115 120 125

Thr Gly Thr Met Pro Pro Leu Pro Leu Glu Ala Thr Gly Leu Ala Leu  
130 135 140

Ser Ser Leu Arg Leu Arg Asn Val Ser Trp Ala Thr Gly Arg Ser Trp  
145 150 155 160

Leu Ala Glu Leu Gln Gln Trp Leu Lys Pro Gly Leu Lys Val Leu Ser  
165 170 175

Ile Ala Gln Ala His Ser Pro Ala Phe Ser Tyr Glu Gln Val Arg Ala  
180 185 190

Phe Pro Ala Leu Thr Ser Leu Asp Leu Ser Asp Asn Pro Gly Leu Gly  
195 200 205

Glu Arg Gly Leu Met Ala Ala Leu Cys Pro His Lys Phe Pro Ala Ile  
210 215 220

Gln Asn Leu Ala Leu Arg Asn Thr Gly Met Glu Thr Pro Thr Gly Val  
225 230 235 240

Cys Ala Ala Leu Ala Ala Gly Val Gln Pro His Ser Leu Asp Leu  
245 250 255

Ser His Asn Ser Leu Arg Ala Thr Val Asn Pro Ser Ala Pro Arg Cys  
260 265 270

Met Trp Ser Ser Ala Leu Asn Ser Leu Asn Leu Ser Phe Ala Gly Leu  
275 280 285

Glu Gln Val Pro Lys Gly Leu Pro Ala Lys Leu Arg Val Leu Asp Leu  
290 295 300

6/9

Ser Cys Asn Arg Leu Asn Arg Ala Pro Gln Pro Asp Glu Leu Pro Glu  
305 310 315 320

Val Asp Asn Leu Thr Leu Asp Gly Asn Pro Phe Leu Val Pro Gly Thr  
325 330 335

Ala Leu Pro His Glu Gly Ser Met Asn Ser Gly Val Val Pro Ala Cys  
340 345 350

Ala Arg Ser Thr Leu Ser Val Gly Val Ser Gly Thr Leu Val Leu Leu  
355 360 365

Gln Gly Ala Arg Gly Phe Ala  
370 375

<210> 6  
<211> 366  
<212> PRT  
<213> murine

<400> 6  
Met Glu Arg Val Leu Gly Leu Leu Leu Leu Leu Val His Ala Ser  
1 5 10 15

Pro Ala Pro Pro Glu Pro Cys Glu Leu Asp Glu Glu Ser Cys Ser Cys  
20 25 30

Asn Phe Ser Asp Pro Lys Pro Asp Trp Ser Ser Ala Phe Asn Cys Leu  
35 40 45

Gly Ala Ala Asp Val Glu Leu Tyr Gly Gly Arg Ser Leu Glu Tyr  
50 55 60

Leu Leu Lys Arg Val Asp Thr Glu Ala Asp Leu Gly Gln Phe Thr Asp  
65 70 75 80

Ile Ile Lys Ser Leu Ser Leu Lys Arg Leu Thr Val Arg Ala Ala Arg  
85 90 95

Ile Pro Ser Arg Ile Leu Phe Gly Ala Leu Arg Val Leu Gly Ile Ser  
100 105 110

Gly Leu Gln Glu Leu Thr Leu Glu Asn Leu Glu Val Thr Gly Thr Ala  
115 120 125

Pro Pro Pro Leu Leu Glu Ala Thr Gly Pro Asp Leu Asn Ile Leu Asn  
130 135 140

Leu Arg Asn Val Ser Trp Ala Thr Arg Asp Ala Trp Leu Ala Glu Leu  
145 150 155 160

Gln Gln Trp Leu Lys Pro Gly Leu Lys Val Leu Ser Ile Ala Gln Ala  
165 170 175

His Ser Leu Asn Phe Ser Cys Glu Gln Val Arg Val Phe Pro Ala Leu  
180 185 190

7/9

Ser Thr Leu Asp Leu Ser Asp Asn Pro Glu Leu Gly Glu Arg Gly Leu  
195 200 205

Ile Ser Ala Leu Cys Pro Leu Lys Phe Pro Thr Leu Gln Val Leu Ala  
210 215 220

Leu Arg Asn Ala Gly Met Glu Thr Pro Ser Gly Val Cys Ser Ala Leu  
225 230 235 240

Ala Ala Ala Arg Val Gln Leu Gln Gly Leu Asp Leu Ser His Asn Ser  
245 250 255

Leu Arg Asp Ala Ala Gly Ala Pro Ser Cys Asp Trp Pro Ser Gln Leu  
260 265 270

Asn Ser Leu Asn Leu Ser Phe Thr Gly Leu Lys Gln Val Pro Lys Gly  
275 280 285

Leu Pro Ala Lys Leu Ser Val Leu Asp Leu Ser Tyr Asn Arg Leu Asp  
290 295 300

Arg Asn Pro Ser Pro Asp Glu Leu Pro Gln Val Gly Asn Leu Ser Leu  
305 310 315 320

Lys Gly Asn Pro Phe Leu Asp Ser Glu Ser His Ser Glu Lys Phe Asn  
325 330 335

Ser Gly Val Val Thr Ala Gly Ala Pro Ser Ser Gln Ala Val Ala Ieu  
340 345 350

Ser Gly Thr Leu Ala Leu Leu Gly Asp Arg Leu Phe Val  
355 360 365

<210> 7  
<211> 377  
<212> PRT  
<213> rabbit

<400> 7  
Met Glu Pro Val Pro Cys Leu Leu Leu Leu Leu Pro Xaa Leu Leu  
1 5 10 15

Arg Ala Ser Thr Asp Thr Pro Glu Pro Cys Glu Leu Asp Asp Asp Asp  
20 25 30

Ile Arg Cys Val Cys Asn Phe Ser Asp Pro Gln Pro Asp Trp Ser Ser  
35 40 45

Ala Leu Gln Cys Met Pro Ala Val Gln Val Glu Met Trp Gly Gly Gly  
50 55 60

His Ser Leu Glu Gln Phe Leu Arg Gln Ala Asp Leu Tyr Thr Asp Gln  
65 70 75 80

Arg Arg Tyr Ala Asp Val Val Lys Ala Leu Arg Val Arg Arg Leu Thr  
85 90 95

8/9

Val Gly Ala Val Gln Val Pro Ala Pro Leu Leu Leu Gly Val Leu Arg  
100 105 110

Val Leu Gly Tyr Ser Arg Leu Lys Glu Leu Ala Leu Glu Asp Ile Glu  
115 120 125

Val Thr Gly Thr Ala Pro Pro Pro Pro Leu Glu Ala Thr Gly Pro  
130 135 140

Ala Leu Ser Thr Leu Ser Leu Arg Asn Val Ser Trp Pro Lys Gly Gly  
145 150 155 160

Ala Trp Leu Ser Glu Leu Gln Gln Trp Leu Lys Pro Gly Leu Gln Val  
165 170 175

Leu Asn Ile Ala Gln Ala His Thr Leu Ala Phe Ser Cys Glu Gln Val  
180 185 190

Arg Thr Phe Ser Ala Leu Thr Thr Leu Asp Leu Ser Glu Asn Pro Gly  
195 200 205

Leu Gly Glu Arg Gly Leu Val Ala Ala Leu Cys Pro His Lys Glu Pro  
210 215 220

Ala Leu Gln Asp Leu Ala Leu Arg Asn Ala Gly Met Lys Ile Leu Gln  
225 230 235 240

Gly Val Cys Ala Ala Leu Ala Glu Ala Gly Val Gln Pro His His Leu  
245 250 255

Asp Leu Ser His Asn Ser Leu Arg Xaa Xaa Xaa Ala Xaa Asp Thr Gln  
260 265 270

Arg Cys Ile Trp Pro Ser Ala Leu Asn Ser Leu Asn Leu Ser Phe Thr  
275 280 285

Gly Leu Gln Gln Val Pro Lys Gly Leu Pro Ala Lys Leu Asn Val Leu  
290 295 300

Asp Leu Ser Cys Asn Lys Leu Asn Arg Ala Pro Gln Pro Gly Glu Leu  
305 310 315 320

Pro Lys Val Val Asn Leu Ser Leu Asp Gly Asn Pro Phe Leu Val Pro  
325 330 335

Gly Ala Ser Lys Leu Gln Glu Asp Leu Thr Asn Ser Gly Val Phe Pro  
340 345 350

Ala Cys Pro Pro Ser Pro Leu Ala Met Gly Met Ser Gly Thr Leu Ala  
355 360 365

Leu Leu Gln Gly Ala Arg Gly Phe Ile  
370 375

<210> 8  
<211> 1405  
<212> DNA  
<213> bovine

<400> 8  
gcgtgacgca ctgtaaagga aagaatccac agtccagccc gacaaccaga gagagaggca

60

9/9

caggctctga	aatctactg	actatgttct	tggggccgaa	gcgtgggcta	tttggggact	120
taggaacagg	cttggccgc	cctgacacctc	gctgtcgccc	cagggtgtcg	tgcctacact	180
gctgctgctg	ctgctgccgt	cactgctgctg	tgtgtctgctg	gacacaacag	aaccctgcga	240
gctggacgac	cacgatttcc	gttgtgtctg	caacttcacg	gatccgaagc	ctgactggtc	300
tagcgccgtt	cagtgttatgg	ttgcccgtcga	ggtgagatc	agtgccggcg	gccgcagcct	360
ggaacagttt	ctcaaggggag	ccgacaccaa	cccgaaagcag	tatgctgaca	caatcaaggc	420
tctgcgcgtt	cggcgactca	agctgggcgc	tgcacaggtt	cctgctcagc	ttctggtcgc	480
cgttctgcgc	gcgctcggtt	actctcgctc	caaggaactg	acgcttgagg	acctggaggt	540
aaccggccca	acgcccccca	cgcctctgga	agccgctggg	cctgcgctca	ccaccctcag	600
tctgcgttaac	gtatcggttga	caacaggagg	tgcctggctc	ggcgaactgc	agcagtgcct	660
caaggctggg	ctcagggtgc	tgaacattgc	ccaagcacac	tcgcttgccct	ttccgtgcgc	720
agggctctcc	accttcgagg	cgctcaccac	cctagacctg	tctgacaatc	ccagtctcgg	780
cgacagcggg	ctgatggcag	ctctctgtcc	gaacaagttc	ccggccctcc	aatatctagc	840
gctacgcaac	gcggggatgg	agacgcccag	cggcgtgtgc	gcggcgctgg	cggcagcgg	900
ggtgcagccc	caaagcctgg	acctcagcca	caactcgctg	cgcgtcaccg	ccccgggtgc	960
tacccgatgt	gtctggccca	gtgcactaag	gtctctcaat	ttgtcggtcg	ctgggcttgg	1020
gcaagtgcct	aagggactgc	cccctaagct	cagcgtgttt	gatctcagct	gcaacaagct	1080
aagcagggag	ccgcggcgg	acgagctgcc	cgaggtaaat	gacctgactc	tggacggaaa	1140
tccctttctg	gaccctggag	ccctccagca	ccaaaatgac	ccgatgatct	ccggcggtgg	1200
cccagcctgt	gcgcgttctg	ccttgaccat	gggggtgtca	ggagccctgg	cgctgcttca	1260
aggagcccga	ggcttcgcgt	aaggccaggg	gaagagaggg	aagaggaatg	aattggctca	1320
gattgccctg	gctccgggag	accctcgcca	ggacatctca	accaaccagc	cttctgtcccc	1380
atccttatta	aaatcttaaa	cagca				1405